ABSTRACT

The present invention is to provide a system for measuring the similarity between protein profile matrices which is suitably used for predicting a

5   protein three-dimensional structure.   The present invention provides a system for measuring the similarity between protein profile matrices, wherein said profile matrix consists of a group of profile columns containing occurrence probabilities every amino acid type at a respective locations of amino acid residues in a multiple alignment in which amino

10   acid sequences in a plurality of related proteins are aligned in multiple, said system for measuring the similarity comprises (a) means for preparing two profile matrices of a query profile matrix and a subject profile matrix; (b) means for calculating correlation coefficients between the respective profile columns in said query profile matrix and the respective profile columns in

15   said subject profile matrix with respect to full or partial combinations of both the respective profile columns; and (c) means for forming a score matrix consisting of said correlation coefficients.